

Bayesian estimation of direct and correlated response to genetic selection on linear feed efficiency (RFI) or feed efficiency as a ratio trait (FCR)

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Efficiency in nutrient utilization by livestock is of great importance in animal breeding programs

Classical Measure of efficiency

output

input

Milk (Milk component)Yeild

Dry matter intake

body weight gain

feed consumption

In breeding programs:

Inverse of efficiency

$$FCR = \frac{\text{Average daily feed intake}}{\text{Average daily gain}}$$

Disadvantages of ratio traits

LINEAR INDEX SELECTION TO IMPROVE TRAITS DEFINED AS RATIOS

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Difficulty in prediction of the effects of genetic selection on FCR in future generations as well as its effect on the production traits in the breeding program.

Distribution of FCR is dependent on the means and (co)variances of its component traits (ADFI and ADG)

Linear feed efficiency

- **Koch et al. (1963): $RFI = FI - E(FI)$**
- $E(FI)$: based on BW and BWG and (maybe) carcass composition (LMP).

• **Kennedy et al. (1993):**

- IF genetic (co)variances are known for FI, BW, BWG, LMP.
Genetic RFI can be estimated

$$\text{var} \begin{bmatrix} y_r \\ y_p \end{bmatrix} = \begin{bmatrix} 1 & -b \\ 0 & 1 \end{bmatrix} \begin{bmatrix} \text{var}(y_f) & \text{cov}(y_f, y_p) \\ \text{cov}(y_f, y_p) & \text{var}(y_p) \end{bmatrix} \begin{bmatrix} 1 & 0 \\ -b & 1 \end{bmatrix}$$

Bayesian analysis

- Integrates unknown population parameters and “fixed” environmental effects and handles properly ratio traits

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Original article

Bayesian analysis of genetic change due to selection using Gibbs sampling

DA Sorensen¹, CS Wang², J Jensen¹, D Gianola²



• Traits

- ADFI: 2.61 (0.39) kg/d
- ADG: 1.12 (0.15) kg/d
- LMP: 62.7 (1.97) percent



The MAXGRO™ terminal line

Statistical model: Bayesian analysis

$$y_{ijkl}^{ADFI} = \text{Gender}_{ij} + \text{Parity}_{ik} + YS_{il} + b^{ADFI}(SBW_i) + a_i^{ADFI} + pe_i^{ADFI} + e_{ijkl}^{ADFI}$$

$$y_{ijkl}^{ADG} = \text{Gender}_{ij} + \text{Parity}_{ik} + YS_{il} + b^{ADG}(SBW_i) + a_i^{ADG} + pe_i^{ADG} + e_{ijkl}^{ADG}$$

$$y_{ijkl}^{LMP} = \text{Gender}_{ij} + \text{Parity}_{ik} + YS_{il} + b^{LMP}(EBW_i) + a_i^{LMP} + pe_i^{LMP} + e_{ijkl}^{LMP}$$

Flat uninformative priors were assumed for all “fixed” effects in the model and for all (co)variance components.

$$\text{Var} \begin{pmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{pmatrix} = \mathbf{I} \otimes \mathbf{R}_0$$

$$\text{Var} \begin{pmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{a}_3 \end{pmatrix} = \mathbf{A} \otimes \mathbf{G}_0$$

RFI estimation

Genetic RFI (RFI_g)

$$a_i^{RFI_g} = a_i^{ADFI} - b_{g.1} a_i^{ADG} - b_{g.2} a_i^{LMP}$$

Phenotypic RFI (RFI_p)

$$a_i^{RFI_p} = a_i^{ADFI} - b_{p.1} a_i^{ADG} - b_{p.2} \hat{a}_i^{LMP}$$

$$\begin{bmatrix} \mathbf{G}_{RFI} & \mathbf{G}_{RFI,p} \\ \mathbf{G}_{p,RFI_g} & \mathbf{G}_p \end{bmatrix} = \mathbf{B} \mathbf{G} \mathbf{B}'$$

$$\begin{bmatrix} \mathbf{P}_{RFI} & \mathbf{P}_{RFI,p} \\ \mathbf{P}_{p,RFI} & \mathbf{P}_p \end{bmatrix} = \mathbf{B} \mathbf{P} \mathbf{B}'$$

$$\mathbf{B} = \begin{bmatrix} \mathbf{I}_{fi} & -\mathbf{b}_{fi p} \\ 0 & \mathbf{I}_p \end{bmatrix}; \mathbf{b}_{g_{fi p}} = \mathbf{G}_p^{-1} \mathbf{G}_{p,fi}; \text{ or } \mathbf{b}_{p_{fi p}} = \mathbf{P}_p^{-1} \mathbf{P}_{p,fi}$$

Breeding values for FCR

The breeding value for FCR is dependent on the fixed effects since it depends on the mean of the traits involved in the ratio (μ_{ADFI} and μ_{ADG}).

$$\alpha_i^{FCR} = \frac{\mu_{ADFI} + \hat{a}_i^{ADFI}}{\mu_{ADG} + \hat{a}_i^{ADG}} - \frac{\mu_{ADFI}}{\mu_{ADG}}$$

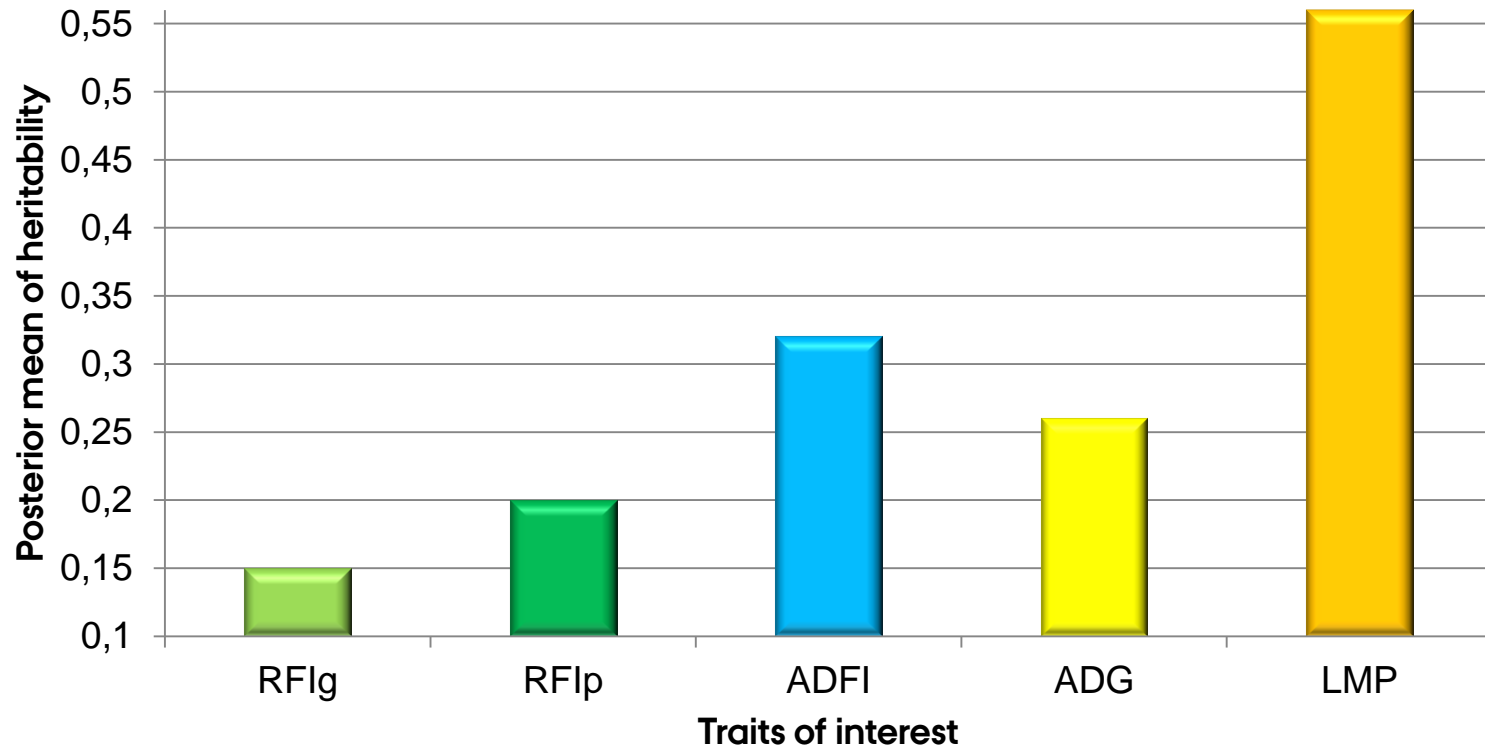
$$\mu_{ADFI} = \frac{\mathbf{1}'\mathbf{b}_1}{rank(\mathbf{X})} + b_{1.1}\bar{S}$$

$$\mu_{ADG} = \frac{\mathbf{1}'\mathbf{b}_2}{rank(\mathbf{X})} + b_{2.1}\bar{S}$$

where $\mathbf{1}$ is a vector of ones, $rank(\mathbf{X})$ in this case is the number of elements in \mathbf{b}_1 or \mathbf{b}_2 ; and \bar{S} is the population average of start BW

Bayesian response to selection

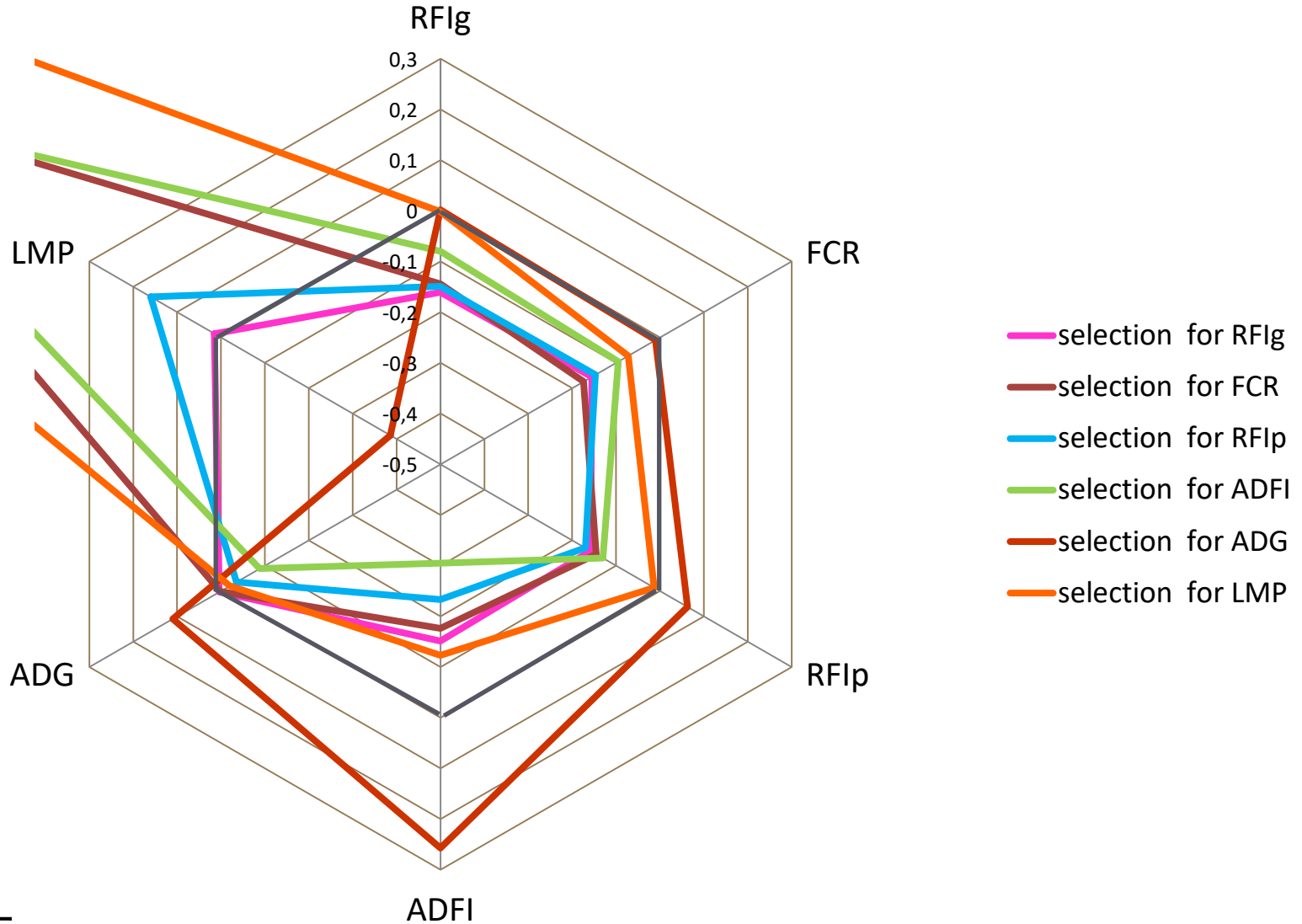
Difference between mean of EBV in the selected population compared to the whole population in each iteration = posterior distribution of response to selection



26.45% with 5.58 PSD of the genetic variation in ADFI is explained by RFI_g.

Selection for RFI results in reduction of ADFI without altering the production traits

Selection for FCR results in disproportional selection on its component traits



Selection for FCR results in disproportional selection pressure on its component traits and also LMP

RFI_g allows

- 1) selection on the proportion of feed intake that is independent of production; and*
- 2) easier and better selection index weights for the traits in the breeding programs*

Selection for improved feed efficiency is likely best achieved through multiple-trait selection on RFI_g and production traits

Joint selection for feed intake and production traits can also result in genetic improvement of feed efficiency



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